FIG. 1

2/24

FIG. 2A   FIG. 2B   FIG. 2C   FIG. 2D   FIG. 2E

3/24

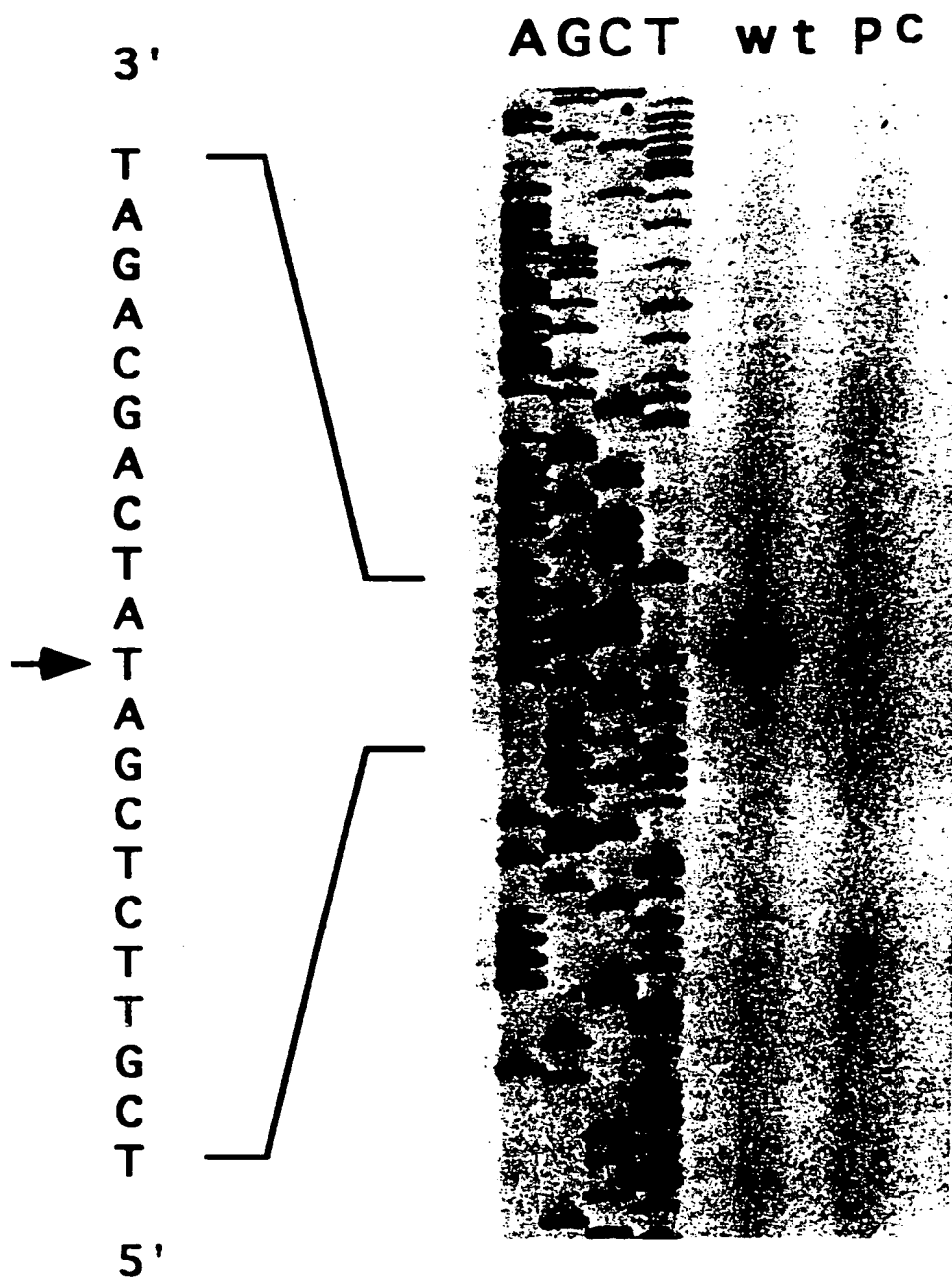**FIG. 3**

4/24

```
              *  **          +* **   ** * * **   ** *****+*  +* +
PrgI  1   ..MATPWSGY........LDDVSAKFDTGVDNLQTQVTEALDKLAAKPSDP   41
MxiH  1   MSVTVPNDDWT.......LSSLSETFDDGTQTLQGELTLALDKLAKNPSNP   44
YscF  1   ...MSNFSGFTKGNDIADLDAVAQTLKKPADDANKAVNDSIAALKDTPDNP   48

          *+++  *+******  ***+**+**+**  ++  ***+*+*+*
PrgI  42  ALLAAYQSKLSEYNLYRNAQSNTVKVFKDIDAAIIQNFR   80  SEQ ID NO:32:
MxiH  45  QLLAEYQSKLSEYTLYRNAQSNTVKVIKDVDAAIIQNFR   83  SEQ ID NO:33:
YscF  49  ALLADLQHSINKWSVIYNISSTIVRSMKDLMQGILQKFP   87  SEQ ID NO:34:
```

FIG. 4A

```
          +  +  +  +  +    +      + +   + ++  +        +          +
PrgJ  1   MSIATIVPENAV.IGQAVNIRSMETDIVSLDDRLLQAFSGSAIATAVDKQT   50
MxiI  1   ..MNYIYPVNQVDIIKASDFQSQE..ISSLEDVVSAKYSDIKMDTDIQVSQ   47

          +      +      +  ++   +    + +       ++      ++ ++ +  ++++++  +        SEQ ID
PrgJ  51  ITNRIEDPNLVTDPKELAISQEMISDYNLYVSMVSTLTRKGVGAVETLLRS  101  NO:35
MxiI  48  IMEMVSNPESL.NPESLAKLQTTLSNYSIGVSLAGTLARKTVSAVETLLKS   97  SEQ ID
                                                                      NO:36
```

FIG. 4B

```
          ***   *  *  +***+ ++*    *+  ** + **++ ****  *** + +
PrgK  1   .MIRRYLYTFLLVMTLAGCKDK.DLLKGLDQEQANEVIAVLQMHNIEANKI   49
MxiJ  1   .MIRYKGFILFLLLMLIGCEQREELISNLSQRQANEIISVLERHNITARKV   50
YscJ  1   MKVKTSLSTLILILFLTGCK..VDLYTGISQKEGNEMLALLRQEGLSADKE   49

          *  ** *  *   +  *  **    +*     *  +  *+   ** *  **++  +*+*++++*
PrgK  50  DSGKLGYSITVAEPDFTAAVYWIKTYQLPPRPRVEIAQMFPADSLVSSPR   99
MxiJ  51  DGGKQGISVQVEKGTFASAVDLMRMYDLPNPERVDISQMFPTDSLVSSPR  100
YscJ  50  PDKDGKIKLLVEESDVAQAIDILKRKGYPHESFSTLQDVFPKDGLISSPI   99

          *+*++++*+**+*+****+    +++*+**+ ***     *  *     ** * +
PrgK  100 AEKARLYSAIEQRLEQSLQTMEGVLSARVHISYDIDAGENGRPPKPVHLS  149
MxiJ  101 AEKARLYSAIEQRLEQSLVSIGGVISAKIHVSYDLE..EKNISSKPMHIS  148
YscJ  100 EELARLNYAKAQEISRTLSEIDGVLVARVHVVLPEEQNNKGKKGVAASAS  149

            *  *           **  ++*****+**  **  +**+++  +       *       *
PrgK  150 ALAVYERGSPLAHQISDIKRFLKNSFADVDYDNISVVL....SERSDAQL  195
MxiJ  149 VIAIYDSPKESELLVSNIKRFLKNTFSDVKYENISVIL....TPKEEYVY  195
YscJ  150 VFIKHAADIQFDTYIPQIKQLVNNSIEGLAYDRISVILPSVDVRQSSHL   199

            *   **      * * +* ****     +* *        +
PrgK  196 Q..APGTPVKRNSFATSWIVLIILLSVMSAGFGVWYYKNHYARNKKGITA  243  SEQ ID
MxiJ  196 TNVQPVKEVKSEFLTNEVIYLFLGMAVLVVILLVWAFKTGWFKRNKI     242  NO:37
YscJ  200 P..RNTSILSIQVSEESKGRLIGLLSLLILLLPVTNLAQYFWLQRKK     244  SEQ ID
                                                                      NO:38
PrgK  243 DDKAKSSNE   252   SEQ ID NO:39
```
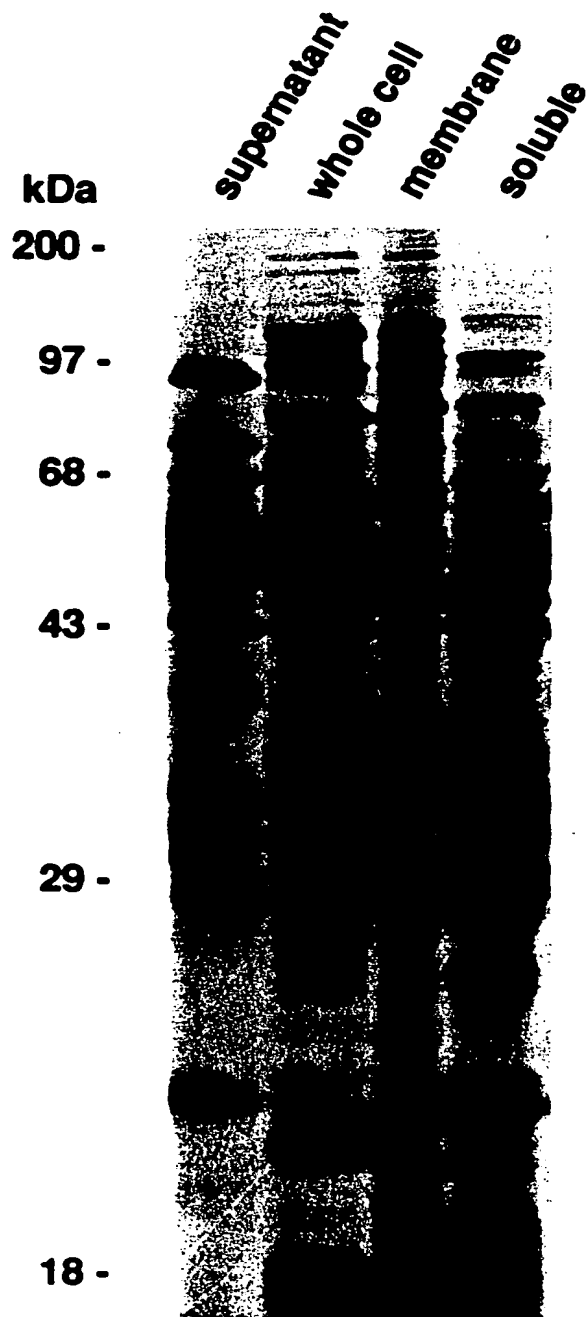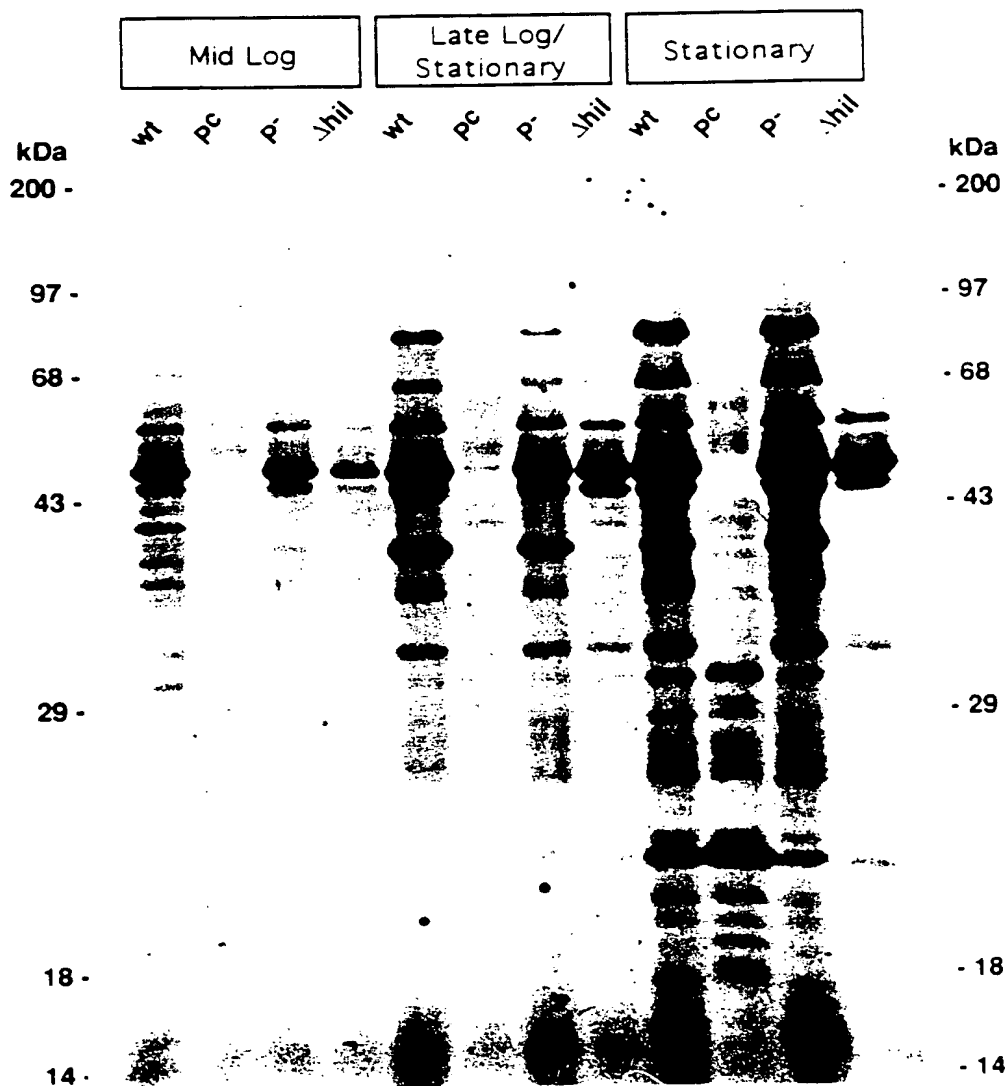
FIG. 4C

5/24

FIG. 5

6/24

FIG. 6

7/24

FIG. 7

8/24

FIG. 8

FIG. 9

	INVASION [% of inoculum]	Ssp A (87)	C (42)	D (36)
SL1344	17.5 ± 2.6	+	+	+
EE633	23.2 ± 3.5	−	+	+
EE638	0.1 ± 0.05	−	−	−

spaT sspB* sspC sspD sspA*   hilA   prgH

1kb

lacZY4

lacZY11-6

FIG. 10

	INVASION [% of inoculum]	Ssp A (87)	C (42)	D (36)
EE638 [pCH002]	7.1 ± 2.3	+	+	+
EE638 [pCH004]	0.2 ± 0.09	−	+	−
EE638 [pCH005]	16.5 ± 2.7	−	+	+
EE638 [pCH006]	0.1 ± 0.05	−	−	+

P_lac

10/24

FIG. 11

```
SspB     RKAEETNRIMGCIGKVLGALLTIVSVVAAVFTGGASLALAAVGLAVMVADEIVKAATGVSFIQQALNPIMEHVLKPLMELIGKAITKALEGLGVDKKTAE
         |||| || ||| |||||| ||||||||||| | |||||||||||||| || |||| ||| || |||||||||| ||| ||| ||||||||| |||| | |
IpaB 298 RKAEELNRVMGCVGKIILGALLTIVSVVAAAFSGGASLALAAVGLALMVTDAIVQAATGNSFMEQALNPIMKAVIEPLIKLLSDAFTKMLEGLGVDSKKAK

SspB     MAGSIVGAIVAAIAMVAVIVVVAVVGKGAAAKIGNALSKMMGETIKKLVPNVLKQLAQNGSKLFTQGMQRITSGLGNVGSKMGLQTNALSKELVGNTLNK
         | ||| ||| ||  | |  ||  | | || ||||||| ||  |||
IpaB 398 MIGSILGAIAGALVLVAAVVLVATVGKQAAAKLAENIGKIIGKTLTDLIPKFLKNFSSQLDDLITNAVARLNKFLGAAGDEV......ISKQIISTHLNQ

SspB     VALGMEVTNTAAQSAGGVAEGVFIKNASEALADFMLARFAMDQIQQWLKQSVEIFGENQKVTAELQKAMSSAVQQNADASRFILRQSRA     SEQ ID NO:40
         | | ||  | | | || |    |  |||      |  |    ||
IpaB 492 AVLLGESVNSATQAGGSVASAVFQNSASTNLADLTLSKYQVEQLSKYISEAIEKFGQLQEVIADLLASMSNSQANRTDVAKAILQQTTA 580 SEQ ID NO:41
```

FIG. 12

```
SspC   1                                    MLISNVGINPAAYLNNHSVENSSQTASQSVSAKDILNSIGI.SSSKVSDLGLSPTLSAPAPGVLTQTPGTITSFLKASIQNTDMNQDLNAL
                                              |     |     |    | ||    |    ||     | |||      |           |    |||
IpaC   1 MLQKQFCNKLLLDTNKENVMEIQN....TKPTQTLYTDISTKQTQSSETQKSQNYQQIAAHIPLNVGKNPVLTTLND.DQLLKLSEQVQHDSEIIARL

SspC  91 ANNVTTKANEVVQTQLREQQAEVGKFFDISGMSSSAVALLAAANTLMLTLNQADSKLSGKLSLVSFDAAKTTASSMREGMNALSGSISQSALQLGITGV
                    |     | ||     || || |||  ||| | |||  ||| ||| |||  || |||     |        |   |     ||||
IpaC  96 TDKKMKDLSEMSHTLTPENT......LDISSLSSNAVSLIISVAVLLSALRTAETKIGSQLSLIAFDATKSAAENIVRQGLAALSSSITGAVTQVGITGI

SspC 191 GAKLEYKGLQNERGALKHNAAKIDKLTTESHSIKNVLNGQNSVKLGAEGVDSLKSLNMKKTGTDATKNLNDATLKSNAGTSATESLGIKDSNKQISPEIIQ
         ||| |   |    | | ||  |  |       |                                                         |||
IpaC 190 GAKKTHSGISDQKGALRKNLATAQSLEKELAGSKLGLNKQIDTNITSPQTNS............STKFLGKNKLAPD.........NISLSTEHK

SspC 291 AILSKRLESVESDIRLEQNTMDMTRIDARRKMQMTGDLIMKNSVTVGGIAGASGQYAATQERSEQQISQVNNRVASTASDEARESSRKSTSLIQEMLKTME
            ||   |   |      ||            |  ||    |  |||  |||| || |||||  ||||      |           ||   ||   |||
IpaC 264 TSLSSPDISLQDKIDTQRRTYELNTLSAQQKQNIGRATMETSAVAGNISTSGGRYASALEEEQLISQASSKQAEEASQVSKEASQATNQLIQKLLNIID

SspC 391 SINQSKASALAAIAGNIRA 409  SEQ ID NO:42
         ||||||  ||   |||||||
IpaC 364 SINQSKNSAASQIAGNIRA 382  SEQ ID NO:43
```

FIG. 13

12/24

```
SspD    1  MLNIQNYSASPHPGIVAERRQTPSASEHVETAVVPSTTEHRGTDIISLSQAATKIHQAQQTLQ...STPPISEENNDERTLARQLTSSLNALAKSGVSL
                 ||   |    |                      |    |   |   |                 |        |    |             |
IpaD    1  MNITTLTNSISTSSFSPNNTNGSSTETVNSDIKTTSSHPVSSLTMLNDTLHNIRTTNQALKKELSQKTLTKTSLEEIALHSSQISMDVNKSAQLLDIL

SspD   98  SAEQ...NENLRSAF.SAPTSALFSASPMAQPRTTISDAEIWDMVSQNISAIGDSYLGVYENVVAVYTDFYQAFSDILSKMGGWLLP.GKDGNTVKLDVT
               |     ||          |||   ||  |   | |||  | | |||  ||  ||  |  | | |   || || |   ||   |||
IpaD  100  SRNEYPINKDARELLHSAPKEAELDGDQM......ISHRELWAKIANSINDINEQYLKVYEHAVSSYTQMYQDFSAVLSSLAGWISPGGNDGNSVKLQVN

SspD  193  SLKNDINSLVNKYNQINSNTVLFPAQSGSGVKVATEAEARQWLSELNLPNSCLKSYGSGYVVTVDLTPLQKMVQDIDGLGAPGKDSKLEWDNAKYQAWQS
               |||  |   | ||  |     |      | ||           ||       ||   | |  ||    |          |||||||
IpaD  194  SLKKALEELKEKYK....DKPLYPANNT.....VSQEQANKWLTELGGTIGKVSQKNGGYVVSINMTPIDNMLKSLDNLGGNG...EVVLDNAKYQAWNA

SspD  293  GFKAQEENMKTTLQTLTQKYSNANSLYDNLVKVLSSTISSSLETAKSFLQG 343    SEQ ID NO:44
               || | | || |||| ||||||||| |||||||||||   | ||
IpaD  282  GFSAEDETMKNNLQTLVQKYSNANSIFDNLVKVLSSTISSCTDTDKLFLHF 332    SEQ ID NO:45
```
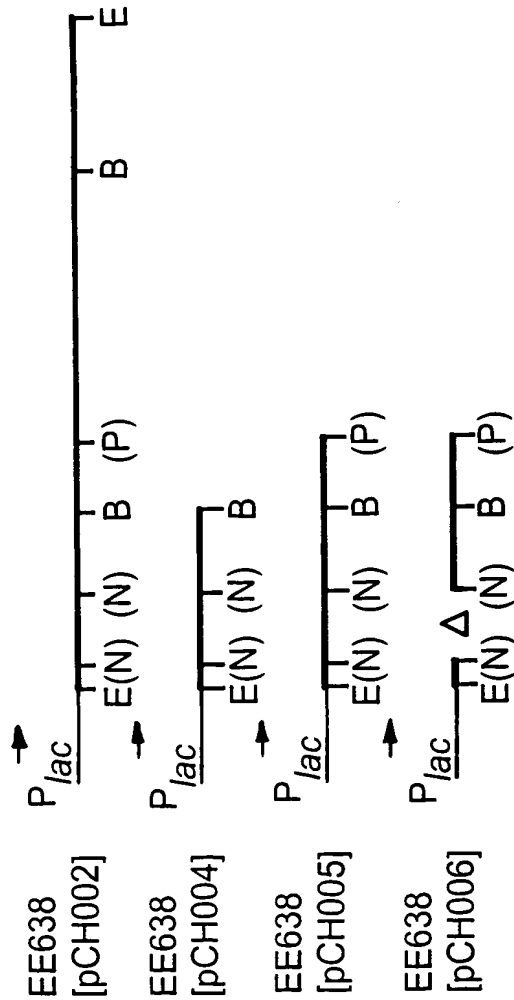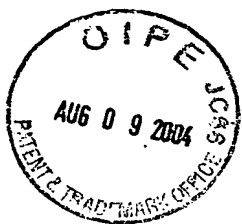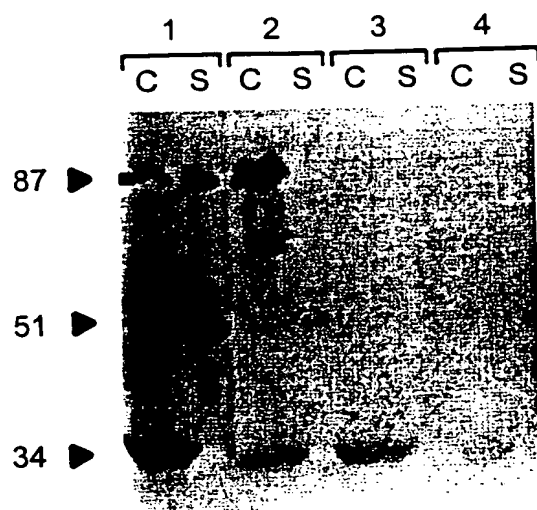
FIG. 14

```
SspA    1  MVTSVRTQPPVIMPGMQTEIKTQATNLAANLSAVRESATATLSGEIKGPQLEDFPALIKQASLD 64    SEQ ID NO:46
```
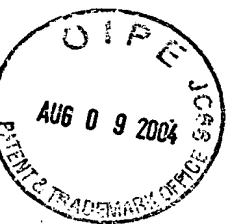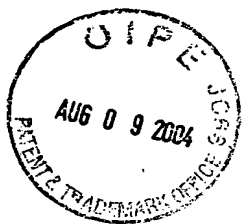
FIG. 15
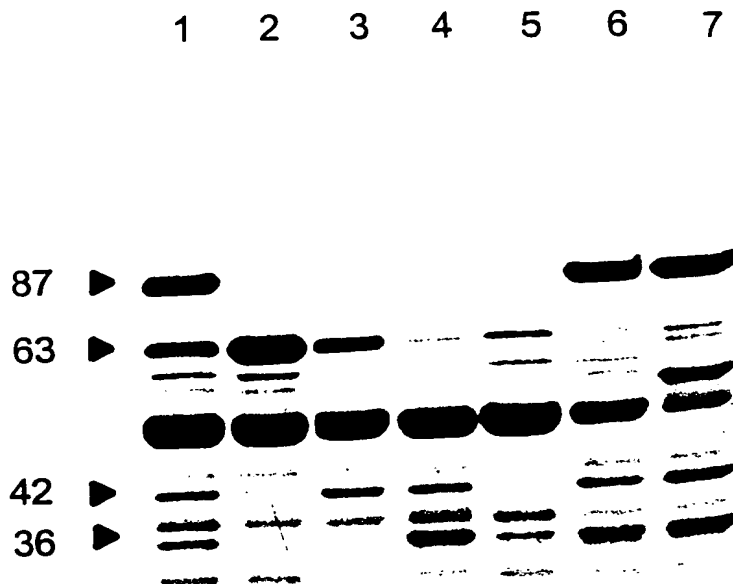
FIG. 16

14/24
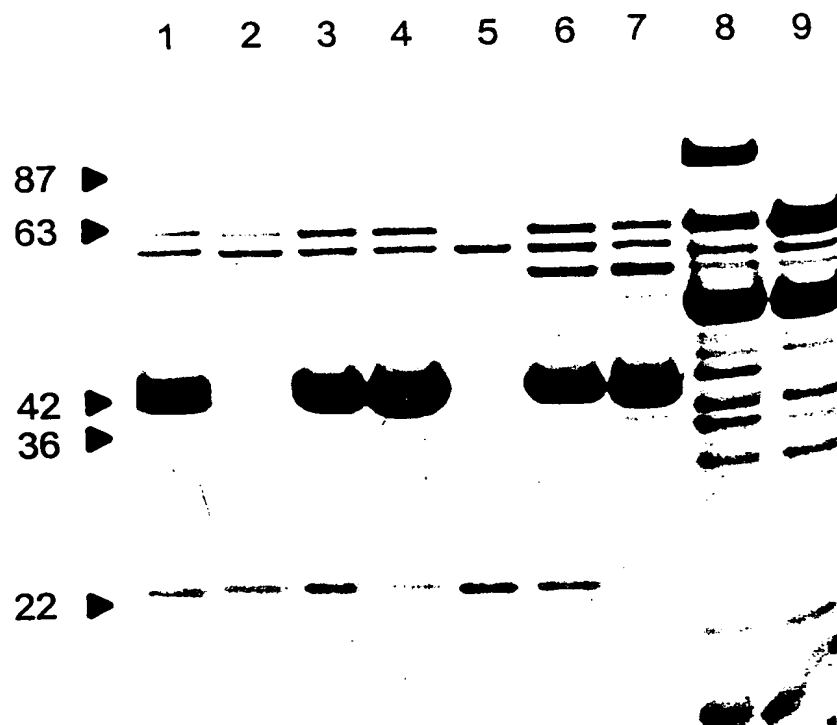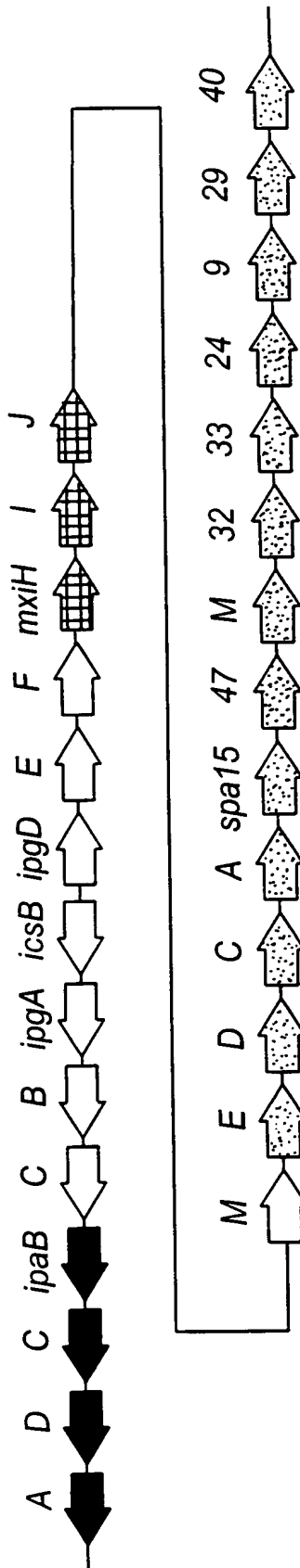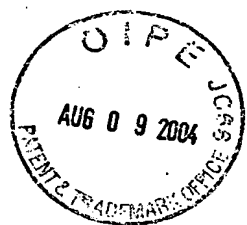

FIG. 17

15/24
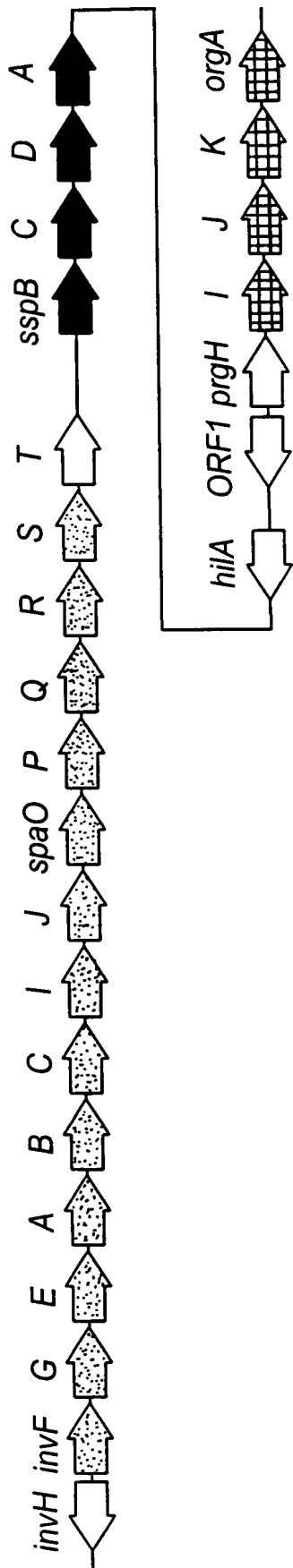
FIG. 18
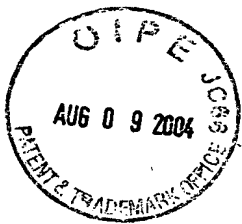
SEQ ID NO:1:

```
CGCAAAGCCG AGGAAACGAA CCGCATTATG GGATGTATCG GGAAAGTCCT CGGCGCGCTG      60
CTAACCATTG TCAGCGTTGT GGCCGCTGTT TTTACCGGTG GGGCGAGTCT GGCGCTGGCT     120
GCGGTGGGAC TTGCGGTAAT GGTGGCCGAT GAAATTGTGA AGGCGGCGAC GGGAGTGTCG     180
TTTATTCAGC AGGCGCTAAA CCCGATTATG GAGCATGTGC TGAAGCCGTT AATGGAGCTG     240
ATTGGCAAGG CGATTACCAA AGCGCTGGAA GGATTAGGCG TCGATAAGAA AACGGCAGAG     300
ATGGCCGGCA GCATTGTTGG TGCGATTGTC GCCGCTATTG CCATGGTGGC GGTCATTGTG     360
GTGGTCGCAG TTGTCGGGAA AGGCGCGGCG GCGAAACTGG GTAACGCGCT GAGCAAAATG     420
ATGGGCGAAA CGATTAAGAC GTTGGTGCCT AACGTGCTGA AACAGTTGGC GCAAAACGGC     480
AGCAAACTCT TTACCCAGGG GATGCAACGT ATTACTAGCG GTCTGGGTAA TGTGGGTAGC     540
AAGATGGGCC TGCAAACGAA TGCCTTAAGT AAAGAGCTGG TAGGTAATAC CCTAAATAAA     600
GTGGCGTTGG GCATGGAAGT CACGAATACC GCAGCCCAGT CAGCCGGTGG TGTTGCCGAG     660
GGCGTATTTA TTAAAAATGC CAGCGAGGCG CTTGCTGATT TTATGCTCGC CCGTTTTGCC     720
ATGGATCAGA TTCAGCAGTG GCTTAAACAA TCCGTAGAAA TATTTGGTGA AAACCAGAAG     780
GTAACGGCGG AACTGCAAAA AGCCATGTCT TCTGCGGTAC AGCAAAATGC GGATGCTTCG     840
CGTTTTATTC TGCGCCAGAG TCGCGCATAA                                      870
```

FIG. 19

SEQ ID NO:2:

```
ATGTTAATTA GTAATGTGGG AATAAATCCC GCCGCTTATT TAAATAATCA TTCTGTTGAG      60
AATAGTTCAC AGACAGCTTC GCAATCCGTT AGCGCTAAAG ATATTCTGAA TAGTATTGGT     120
ATTAGCAGCA GTAAAGTCAG TGACCTGGGG TTGAGTCCTA CACTGAGCGC GCCTGCGCCA     180
GGGGTATTAA CGCAAACCCC CGGAACGATC ACGTCCTTTT TAAAAGCCAG TATTCAAAAT     240
ACCGACATGA ATCAGGATTT GAATGCTCTG GCAAATAATG TCACGACTAA AGCGAATGAG     300
GTTGTGCAAA CCCAGTTACG CGAGCAGCAG GCAGAAGTCG GAAAGTTTTT TGATATTAGC     360
GGAATGTCTT CCAGTGCCGT TGCGCTGTTG GCTGCCGCGA ATACGTTAAT GCTGACGTTG     420
AACCAGGCTG ATAGCAAACT GTCTGGTAAG TTGTCATTAG TCAGTTTTGA TGCAGCTAAA     480
ACGACGGCAA GCTCCATGAT GCGCGAAGGG ATGAATGCGT TGTCCGGTAG TATTTCCCAG     540
AGCGCGCTTC AGTTGGGGAT CACTGGCGTG GGCGCCAAAC TGGAATATAA GGGGCTGCAG     600
AATGAAAGAG GCGCGCTTAA ACATAATGCC GCGAAGATCG ATAAACTGAC CACTGAAAGC     660
CACAGTATTA AAAACGTGCT GAACGGGCAG AATAGCGTCA AACTCGGTGC TGAAGGCGTC     720
GATTCTCTGA ATCGTTAAA TATGAAGAAA ACCGGTACCG ATGCGACGAA AAATCTTAAT     780
GATGCGACGC TTAAATCTAA TGCCGGAACC AGCGCCACGG AAAGTCTGGG TATTAAAGAC     840
AGTAATAAAC AAATCTCCCC TGAACATCAG GCTATTCTGT CGAAACGTCT TGAGTCTGTC     900
GAATCCGATA TTCGTCTTGA GCAGAATACC ATGGATATGA CCCGAATCGA TGCGCGCAAG     960
ATGCAGATGA CGGGCGATCT GATTATGAAG AACTCGGTCA CGGTCGGTGG TATTGCAGGG    1020
GCGTCCGGGC AGTACGCCGC TACTCAGGAA CGTTCCGAGC AGCAAATTAG CCAGGTGAAT    1080
AACCGGGTTG CCAGCACCGC ATCGGACGAA GCCCGTGAAA GTTCACGTAA ATCGACCAGC    1140
CTGATTCAGG AAATGCTGAA AACAATGGAG AGCATTAACC AGTCGAAAGC ATCCGCACTC    1200
GCTGCTATCG CAGGCAATAT TCGCGCTTAA                                     1230
```

FIG. 20

17/24

SEQ ID NO:3:

```
ATGCTTAATA TTCAAAATTA TTCCGCTTCT CCTCATCCGG GGATCGTTGC CGAACGGCCG    60
CAGACTCCCT CGGCGAGCGA GCACGTCGAG ACTGCCGTGG TACCGTCTAC CACAGAACAT   120
CGCGGTACAG ATATCATTTC ATTATCGCAG GCGGCTACTA AAATCCACCA GGCACAGCAG   180
ACGCTGCAGT CAACGCCACC GATCTCTGAA GAGAATAATG ACGAGCGCAC GCTGGCGCGC   240
CAGCAGTTGA CCAGCAGCCT GAATGCGCTG GCGAAGTCCG GCGTGTCATT ATCCGCAGAA   300
CAAAATGAGA ACCTGCGGAG CGCGTTTTCT GCGCCGACGT CGGCCTTATT TAGCGCTTCG   360
CCTATGGCGC AGCCGAGAAC AACCATTTCT GATGCTGAGA TTTGGGATAT GGTTTCCCAA   420
AATATATCGG CGATAGGTGA CAGCTATCTG GGCGTTTATG AAAACGTTGT CGCAGTCTAT   480
ACCGATTTTT ATCAGGCCTT CAGTGATATT CTTTCCAAAA TGGGAGGCTG GTTATTACCA   540
GGTAAGGACG GTAATACCGT TAAGCTAGAT GTTACCTCAC TCAAAAATGA TTTAAACAGT   600
TTAGTCAATA AATATAATCA AATAAACAGT AATACCGTTT TATTTCCAGC GCAGTCAGGC   660
AGCGGCGTTA AAGTAGCCAC TGAAGCGGAA GCGAGACAGT GGCTCAGTGA ATTGAATTTA   720
CCGAATAGCT GCCTGAAATC TTATGGATCC GGTTATGTCG TCACCGTTGA TCTGACGCCA   780
TTACAAAAAA TGGTTCAGGA TATTGATGGT TTAGGCGCGC CGGGAAAAGA CTCAAAACTC   840
GAAATGGATA ACGCCAAATA TCAAGCCTGG CAGTCGGGTT TTAAAGCGCA GGAAGAAAAT   900
ATGAAAACCA CATTACAGAC GCTGACGCAA AAATATAGCA ATGCCAATTC ATTGTACGAC   960
AACCTGGTAA AAGTGCTGAG CAGTACGATA AGTAGCAGCC TGGAAACCGC CAAAAGCTTC  1020
CTGCAAGGAT AA                                                      1032
```

FIG. 21

18/24

ATGGTTACAA GTGTAAGGAC TCAGCCCCCC GTCATAATGC CAGGTATGCA GACCGAGATC
AAAACGCAGG CCACGAATCT TGCGGCGAAT CTTTCCGCAG TCAGAGAAAG TGCCACAGCG
ACGCTGTCAG GGGAAATTAA AGGCCCGCAA CTGGAAGATT TTCCCGCGCT GATCAAACAG
GCGAGTCTGG ATGC   SEQ ID NO:4

RKAEETNRIMGCIGKVLGALLTIVSVVAAVFTGGASLALAAVGLAVMVADEIVKAATGVS
FIQQALNPIMEHVLKPLMELIGKAITKALEGLGVDRKRQRWPAALLVRLSPLCHGDAVIV
VVAVVGKGAAAKLGNALSKMMGETIKKLVPNVLKQLAQNGSKLFTQGMQRITSGLGNVGS
KMGLQTNALSKELVGNTLNKVALGMEVTNTAAQSAGGVAEGVFIKNASEALADFMLARFA
MDQIQQWLKQSVEIFGENQKVTAELQKAMSSAVQQNADASRFILRQSRAZ   SEQ ID NO:5

FIG. 22

19/24

MLISNVGINPAAYLNNHSVENSSQTASQSVSAKDILNSIGISSSKVSDLGLSPTLSAPAP
GVLTQTPGTITSFLKASIQNTDMNQDLNALANNVTTKANEVVQTQLREQQAEVGKFFDIS
GMSSSAVALLAAANTLMLTLNQADSKLSGKLSLVSFDAAKTTASSMMREGMNALSGSISQ
SALQLGITGVGAKLEYKGLQNERGALKHNAAKIDKLTTESHSIKNVLNGQNSVKLGAEGV
DSLKSLNMKKTGTDATKNLNDATLKSNAGTSATESLGIKDSNKQISPEHQAILSKRLESV
ESDIRLEQNTMDMTRIDARKMQMTGDLIMKNSVTVGGIAGASGQYAATQERSEQQISQVN
NRVASTASDEARESSRKSTSLIQEMLKTMESINQSKASAL AAIAGNIRAZ
SEQ ID NO:6

MLNIQNYSASPHPGIVAERPQTPSASEHVETAVVPSTTEHRGTDIISLSQAATKIHQAQQ
TLQSTPPISEENNDERTLARQQLTSSLNALAKSGVSLSAEQNENLRSAFSAPTSALFSAS
PMAQPRTTISDAEIWDMVSQNISAIGDSYLGVYENVVAVYTDFYQAFSDILSKMGGWLLP
GKDGNTVKLDVTSLKNDLNSLVNKYNQINSNTVLFPAQSGSGVKVATEAEARQWLSELNL
PNSCLKSYGSGYVVTVDLTPLQKMVQDIDGLGAPGKDSKLEMDNAKYQAWQSGFKAQEEN
MKTTLQTLTQKYSNANSLYDNLVKVLSSTISSSLETAKSFLQGZ
SEQ ID NO:7

MVTSVRTQPPVIMPGMQTEIKTQATNLAANLSAVRESATATLSGEIKGPQLEDFPALIKQ
ASLD
SEQ ID NO:8

FIG. 23

ATGCATTATTTTTTTATCATCGTAATCTGGTTGCTTAGCATAAATACGGCATGGGCTGAT
TCTGGCTTCAGGCTGAAAAAATGTTCAATATTGAATCCGAACTACTTTACGCTATCGCCCAGCAG
GAATCGGCGATGAAACCTGGCGCCATTGGTCATAACCGAGATGGTTCAACCGATCTTGGCCTGAT
GCAAATTAACAGCTTCCATATGAAAAGGCTGAAAAAAATGGGGATTAGTGAAAAACAGTTGTTAC
AGGACCCCTGCATTTCTGTCATTGTGGGCGACCTCCATTTTATCAGATATGATGAAAATCTACGG
TTATAGCTGGGAGGCCGTTGGCGCTTATAATGCCGGGACGTCGCCGAAACGATCGGATATAAGGA
AACGTTATGCTAAAAAATTTGGGAGAATTACAGAAAATTAAAAGGAATGTCAGCAGAAGAGAAA
AACAAAAGACTTTCTATCGCGGCAAACAAATAA   (SEQ ID NO:9)

ATCAGCTTGCCGTCGTCATAAGCAACTGGGCTTGCATTGCTTTTAGTTGTACAAACTGTGCAGGC
GTCTTCCAGCATTCTATTGTTCCGTGAATCCGGAAATCTGCACGTACCTGCTCCAGATTACTATG
AGGATTATCCTTAAGTACAAGGGCCGCCGCCATCGTTCCGGTTCTTCCCACTCCGCCCAGACAAT
GAATCATCGGTAAATGCTTATCTGATGAACTACGCCCCGGCGCGCCATTTTGGTTACTATTTTTC
ACCCTATCCGCCAGGTATTCTAACTGATCCGTAGACGGTAACGGCTGGTGATCTGGCCAATTTTT
CACATGCAATACCGGGATTGTATACCGCTTTCCCCGCAGGACAGTTGCATATTGTATTGGTCTAT
CGCTTCTCCCTGACTGGCTGAGCTCTCTTTTTGGCTGTTGGTATGCACCTCGCCAAAGGTGTAGC
TCCCTCTGAAATAGGTGGTAATTGTTTTGCCTGCATCTGATCTTCCGACGTTAACACCACCAGGC
ACGAGCATTCTTTTTCAAGAAGCATTTTCATATGCGCTTCCAGCGCATCCCGGCGATTT
(SEQ ID NO:10)

FIG. 24
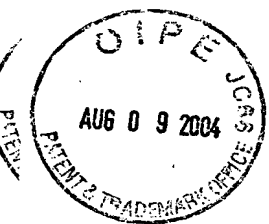
MHYFFIIVIWLLSINTAWADSGFRLKKCSILNPNYFTLSPSRNRRZNLAPLVITEMVQPI
LAZCKLTASIZKGZKKWGLVKNSCYRTPAFLSLWATSILSDMMKIYGYSWEAVGAYNAGT
SPKRSDIRKRYAKKIWENYRKLKGMSAEEKNKRLSIAANK

SEQ ID NO:11

WPGTICGQQHSINQQTQVKLSDGMPVPVIRLTFDGKPVALAGIRTQKIRPDRLEAHMKML
LEKECSCLVVLTSERSDAGKTITTYFRGSYTFGEVHTNSQKVSSASQGEAIDQYNMQLSC
GEKRYTIPVLHVKNWPDHQPLPSTDQLEYLADRVKNSNQNGAPGRSSSDKHLPMIHCLGG
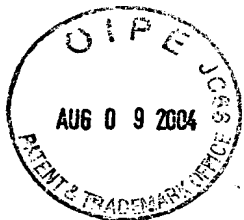VGRTGTMAAALVLKDNPHSNLEQVRADFRIHGTIECWKTPAQFVQLKAMQAQLLMTTAS

SEQ ID NO:12

FIG. 25

MRDCLNNGNPVLNVGASGLTTLPDRLPPHITTLVIPDNNLTSLPELPEGLRELEVSGNLQ
LTSLPSLPQGLQKLWAYNNWLASLPTLPPGLGDLAVSNNQLTSLPEMPPALRELRVSGNN
LTSLRALPSGLQKLWAYNNRLTSLPEMSPGLQELDVSHNQLTRLPQSLTGLSSAARVYLD
GNPLSVRTRDRLCGHHWPFRHQDTLRYGGAFRPREARALHLAVADWLTSAREGEAAQADR
WQAFGLEDNAAAFSLVLDRLRETENFKKDAGFKAQISSWLTQLAEDAALRAKTFAMATEA
TSTCEDRVTHALHQMNNVQLVHNAEKGEYDNNLQGLVSTGREMFRLATLEQIAREKAGTL
ALVDDVEVYLAFQNKLKESLELTSVTSEMRFFDVSGVTVSDLQAADVQVKTAENSGFSKW
ILQWGPLHSVLERKVPERFNALREKQISDYEDTYRKLYDEVLKSSGLVDDTDAERTIGVS
AMDSAKKEFLDGLRALVDEVLGSYLTARWRLNZ

SEQ ID NO:14

FIG. 27

22/24

```
ATGCGTGATT GCCTGAATAA CGGCAATCCA GTGCTTAACG TGGGAGCGTC AGGTCTTACC
ACCTTACCAG ACCGTTTACC ACCGCATATT ACAACACTGG TTATTCCTGA TAATAATCTG
ACCAGCCTGC CGGAGTTGCC GGAAGGACTA CGGGAGCTGG AGGTCTCTGG TAACCTACAA
CTGACCAGCC TGCCATCGCT GCCGCAGGGA CTACAGAAGC TGTGGGCCTA TAATAATTGG
CTGGCCAGCC TGCCGACGTT GCCGCCAGGA CTAGGGGATC TGGCGGTCTC TAATAACCAG
CTGACCAGCC TGCCGGAGAT GCCGCCAGCA CTACGGGAGC TGAGGGTCTC TGGTAACAAC
CTGACCAGCT GCGCGCGCTG CCGTCAGGAC TACAGAAGCT GTGGGCCTAT AATAATCGGC
TGACCAGCCT GCCGGGAGATG TCGCCAGGAC TACAGGAGCT GGATGTCTCT CATAACCAGC
TGACCCGCCT GCCGCAAAGC CTCACGGGTC TGTCTTCAGC GGCACGCGTA TATCTGGACG
GGAATCCACT GTCTGTACGC ACTCGTGACA GGCTCTGCGG ACATCATTGG CCATTCAGGC
ATCAGGATAC ACTTCGATAT GGCGGGGCCT TCCGTCCCCG GGAAGCCCAG GCACTGCACC
TGGCGGTCGC TGACTGGCTG ACGTCTGCAC GGGAGGGGGA AGCGGCCCAG GCAGACAGAT
GGCAGGCGTT CGGACTGGAA GATAACGCCG CCGCCTTCAG CCTGGTCCTG GACAGACTGC
GTGAGACGGA AAACTTCAAA AAAGACGCGG GCTTTAAGGC ACAGATATCA TCCTGGCTGA
CACAACTGGC TGAAGATGCT GCGCTGAGAG CAAAAACCTT TGCCATGGCA ACAGAGGCAA
CATCAACCTG CGAGGACCGG GTCACACATG CCCTGCACCA GATGAATAAC GTACAACTGG
TACATAATGC AGAAAAAGGG GAATACGACA ACAATCTCCA GGGGCTGGTT TCCACGGGGC
GTGAGATGTT CCGCCTGGCA ACACTGGAAC AGATTGCCCG GGAAAAAGCC GGAACACTGG
CTTTAGTCGA TGACGTTGAG GTCTATCTGG CGTTCCAGAA TAAGCTGAAG GAATCACTTG
AGCTGACCAG CGTGACGTCA GAAATGCGTT TCTTTGACGT TTCCGGCGTG ACGGTTTCAG
ACCTTCAGGC TGCGGACGTT CAGGTGAAAA CCGCTGAAAA CAGCGGGTTC AGTAAATGGA
TACTGCAGTG GGGGCCGTTA CACAGCGTGC TGGAACGCAA AGTGCCGGAA CGCTTTAACG
CGCTTCGTGA AAAGCAAATA TCGGATTATG AAGACACGTA CCGGAAGCTG TATGACGAAG
TGCTGAAATC GTCCGGGCTG GTCGACGATA CCGATGCAGA ACGTACTATC GGAGTAAGTG
CGATGGATAG TGCGAAAAAA GAATTTCTGG ATGGCCTGCG CGCTCTTGTG GATGAGGTGC
TGGGTAGCTA TCTGACAGCC CGGTGGCGTC TTAACTGA
```

SEQ ID NO:13

FIG. 26

23/24

```
CGCAAAGCCGAGGAAACGAACCGCATTATGGGATGTATCGGGAAAGTCCTCGGCGCGCTG
CTAACCATTGTCAGCGTTGTGGCCGCTGTTTTTACCGGTGGGGCGAGTCTGGCGCTGGCT
GCGGTGGGACTTGCGGTAATGGTGGCCGATGAAATTGTGAAGGCGGCGACGGGAGTGTCG
TTTATTCAGCAGGCGCTAAACCCGATTATGGAGCATGTGCTGAAGCCGTTAATGGAGCTG
ATTGGCAAGGCGATTACCAAAGCGCTGGAAGGATTAGGCGTCGATAAGAAAACGGCAGAG
ATGGCCGGCAGCATTGTTGGTGCGATTGTCGCCGCTATTGCCATGGTGGCGGTCATTGTG
GTGGTCGCAGTTGTCGGGAAAGGCGCGGCGGCGAAACTGGGTAACGCGCTGAGCAAAATG
ATGGGCGAAACGATTAAGAAGTTGGTGCCTAACGTGCTGAAACAGTTGGCGCAAAACGGC
AGCAAACTCTTTACCCAGGGGATGCAACGTATTACTAGCGGTCTGGGTAATGTGGGTAGC
AAGATGGGCCTGCAAACGAATGCCTTAAGTAAAGAGCTGGTAGGTAATACCCTAAATAAA
GTGGCGTTGGGCATGGAAGTCACGAATACCGCAGCCCAGTCAGCCGGTGGTGTTGCCGAG
GGCGTATTTATTAAAAATGCCAGCGAGGCGCTTGCTGATTTTATGCTCGCCCGTTTTGCC
ATGGATCAGATTCAGCAGTGGCTTAAACAATCCGTAGAAATATTTGGTGAAAACCAGAAG
GTAACGGCGGAACTGCAAAAAGCCATGTCTTCTGCGGTACAGCAAAATGCGGATGCTTCG
CGTTTTATTCTGCGCCAGAGTCGCGCATAAAAACTGCCAAAATAAAGGGAGAAAAAT**ATG**
TTAATTAGTAATGTGGGAATAAATCCCGCCGCTTATTTAAATAATCATTCTGTTGAGAAT
AGTTCACAGACAGCTTCGCAATCCGTTAGCGCTAAAGATATTCTGAATAGTATTGGTATT
AGCAGCAGTAAAGTCAGTGACCTGGGGTTGAGTCCTACACTGAGCGCGCCTGCGCCAGGG
GTATTAACGCAAACCCCCGGAACGATCACGTCCTTTTTAAAAGCCAGTATTCAAAATACC
GACATGAATCAGGATTTGAATGCTCTGGCAAATAATGTCACGACTAAAGCGAATGAGGTT
GTGCAAACCCAGTTACGCGAGCAGCAGGCAGAAGTCGGAAAGTTTTTTGATATTAGCGGA
ATGTCTTCCAGTGCCGTTGCGCTGTTGGCTGCCGCGAATACGTTAATGCTGACGTTGAAC
CAGGCTGATAGCAAACTGTCTGGTAAGTTGTCATTAGTCAGTTTTGATGCAGCTAAAACG
ACGGCAAGCTCCATGATGCGCGAAGGGATGAATGCGTTGTCCGGTAGTATTTCCCAGAGC
GCGCTTCAGTTGGGGATCACTGGCGTGGGCGCCAAACTGGAATATAAGGGGCTGCAGAAT
GAAAGAGGCGCGCTTAAACATAATGCCGCGAAGATCGATAAACTGACCACTGAAAGCCAC
AGTATTAAAAACGTGCTGAACGGGCAGAATAGCGTCAAACTCGGTGCTGAAGGCGTCGAT
TCTCTGAAATCGTTAAATATGAAGAAAACCGGTACCGATGCGACGAAAAATCTTAATGAT
GCGACGCTTAAATCTAATGCCGGAACCAGCGCCACGGAAAGTCTGGGTATTAAAGACAGT
AATAAACAAATCTCCCCTGAACATCAGGCTATTCTGTCGAAACGTCTTGAGTCTGTCGAA
TCCGATATTCGTCTTGAGCAGAATACCATGGATATGACCCGAATCGATGCGCGCAAGATG
CAGATGACGGGCGATCTGATTATGAAGAACTCGGTCACGGTCGGTGGTATTGCAGGGGCG
TCCGGGCAGTACGCCGCTACTCAGGAACGTTCCGAGCAGCAAATTAGCCAGGTGAATAAC
CGGGTTGCCAGCACCGCATCGGACGAAGCCCGTGAAAGTTCACGTAAATCGACCAGCCTG
ATTCAGGAAATGCTGAAAACAATGGAGAGCATTAACCAGTCGAAAGCATCCGCACTCGCT
GCTATCGCAGGCAATATTCGCGCTTAATCTGAAAGGTCATCTATACGCCATCATGGGTGT
GATTTAATCGCGCTCCTGATGGCGAACTGGGGATATT**ATG**CTTAATATTCAAAATTATTC
CGCTTCTCCTCATCCGGGGATCGTTGCCGAACGGCCGCAGACTCCCTCGGCGAGCGAGCA
CGTCGAGACTGCCGTGGTACCGTCTACCACAGAACATCGCGGTACAGATATCATTTCATT
ATCGCAGGCGGCTACTAAAATCCACCAGGCACAGCAGACGCTGCAGTCAACGCCACCGAT
CTCTGAAGAGAATAATGACGAGCGCACGCTGGCGCGCCAGCAGTTGACCAGCAGCCTGAA
TGCGCTGGCGAAGTCCGGCGTGTCATTATCCGCAGAACAAAATGAGAACCTGCGGAGCGC
GTTTTCTGCGCCGACGTCGGCCTTATTTAGCGCTTCGCCTATGGCGCAGCCGAGAACAAC
CATTTCTGATGCTGAGATTTGGGATATGGTTTCCAAAATATATCGGCGATAGGTGACAG
CTATCTGGGCGTTTATGAAAACGTTGTCGCAGTCTATACCGATTTTTATCAGGCCTTCAG
TGATATTCTTTCCAAAATGGGAGGCTGGTTATTACCAGGTAAGGACGGTAATACCGTTAA
GCTAGATGTTACCTCACTCAAAAATGATTTAAACAGTTTAGTCAATAAATATAATCAAAT
AAACAGTAATACCGTTTTATTTCCAGCGCAGTCAGGCAGCGGCGTTAAAGTAGCCACTGA
AGCGGAAGCGAGACAGTGGCTCAGTGAATTGAATTTACCGAATAGCTGCCTGAAATCTTA
TGGATCCGGTTATGTCGTCACCGTTGATCTGACGCCATTACAAAAAATGGTTCAGGATAT
TGATGGTTTAGGCGCGCCGGGAAAAGACTCAAAACTCGAAATGGATAACGCCAAATATCA
AGCCTGGCAGTCGGGTTTTAAAGCGCAGGAAGAAAATATGAAAACCACATTACAGACGCT
GACGCAAAAATATAGCAATGCCAATTCATTGTACGACAACCTGGTAAAAGTGCTGAGCAG
TACGATAAGTAGCAGCCTGGAAACCGCCAAAAGCTTCCTGCAAGGATAACAGAAGAGGAT
ATTAATA**ATG**GTTACAAGTGTAAGGACTCAGCCCCCCGTCATAATGCCAGGTATGCAGAC
CGAGATCAAAACGCAGGCCACGAATCTTGCGGCGAATCTTTCCGCAGTCAGAGAAAGTGC
CACAGCGACGCTGTCAGGGGAAATTAAAGGCCCGCAACTGGAAGATTTTCCCGCGCTGAT
CAAACAGGCGAGTCTGGATGC
```

SEQ ID NO:15

FIG. 28

24/24

```
GAGCTCAGCAACGTGTCGAAAGCCTGTAAAATCATGGGCGTCTCGCGCGATACGTTTTAC
CGTTATCGTGAACTGGCCGATGAAGGCGGCGTTGATGCGCTGATAAATCGTAGTCGCCGC
GTACCTAACCTTAAGAACCGTACCGATGAGGCAACTGAGCAAGCTGTTGTTGATTATGCC
GTTGCGTTCCCGGCCCATGGTCAGCACCGAACTGCGCAAACAGGACGTTTTTATCTCCGG
TAGTGATGTCCATTCCGTCTGGCTGCGCACAACCTTGAGAACTTCAAAAAACGCCTGAAA
GCGCTGGAAGAAAAGTGGCCCGCGATGGCATTGAACTGACTGCCAGATCGCCGCGCTGG
AGCGTAAAGCCAGTGATGATGAAGCCTGTGGTGAGATTGAAACCGTTCATCCGGGATATC
TGGGGTCACAGGACACGTTCTACGTGGGCAACCTGAAAGGCGTTGGGCGAATCTATCAGC
AGACGTTCGTTGATACATACTCGAAGGTGGCTCACTGCAAGCGCTATATCACCAAAACGC
CGATTACAGCGGCTGATTTGCTGAATGATCGTGTACTGCCGTTTATGAGTCTCAGGGCCT
GCCGATGCTAAGGATACTGACAGACAGGGGTACAGAATATTGCGGCAAAGTGGAACATCA
TGATTATCAGCTTTATCTGGAGATAAATGACATCGAACACACGAAAACGAAGGCGATGTC
CCCGCAGACCAATGGCATCTGCGAGCGGTTCCATAAAACGATACTGAACGAATTTTATCA
GGTGACGTTCCGCAAAAAGTTATATGGCGATTTTGATACATTACAATCGGATCTTGATGA
ATGGCTGGTTCACTATAATAATGAGCGAACCCATCAGGGAAAAATGTGCTGTGGCCGGAC
GCCGATGGAAACGTTACTTGATGGAAAACGCATCTGGTCTGAGAAGAATTTAAGCCAGAT
GTAATCTGACAGATACCTGTATAAATAACCGGTAACTGTCAGATCAGGTCTGAGCTAATA
CAACTAATTGTATGTTATTTGTCGTTTATTGCTAAATATATCGTTAATTGAAGGCTTG
ATGCGTGTGTCTGCGTTAATCTCTTTTCATTGTGCTGTAAATTAGGCAGTGGAATATGTT
TAATATCCGCAATACACAACCTTCTGTAAGTATGCAGGCTATTGCTGGTGCAGCGGCACC
AGAGGCATCTCCGGAAGAAATTGTATGGGAAAAATTCAGGTTTTTTTCCCGCAGGAAAAT
TACGAAGAAGCGCAACAGTGTCTCGCTGAACTTTGCCATCCGGCCCGGGGAATGTTGCCT
GATCATATCAGCAGCCAGTTTGCGCGTTTAAAAGCGCTTACCTTCCCCGCGTGGGAGGAG
AATATTCAGTGTAACAGGGATGGTATAAATCAGTTTTGTATTCTGGATGCAGGCAGCAAG
GAGATATTGTCAATCACTCTTGATGATGCCGGGAACTATACCGTGAATTGTCAGGGGTAC
AGTGAAGCACATGACTTCATCATGGACACAGAACCGGGAGAGGAATGCACAGAATTCGCG
GAGGGGGCATCCGGGACATCCCTCCGCCCTGCCACAACGGTTTCACAGAAGGCAGCAGAG
TATGATGCTGTCTGGTCAAATGGGAAAGGGATGCACCAGCAGGAGAGTCACCCGGCCGCG
CAGCAGTGGTACAGGAAATGCGTGATTGCCTGAATAACGGCAATCCAGTGCTTAACGTGG
GAGCGTCAGGTCTTACCACCTTACCAGACCGTTTACCACCGCATATTACAACACTGGTTA
TTCCTGATAATAATCTGACCAGCCTGCCGGAGTTGCCGGAAGGACTACGGGAGCTGGAGG
TCTCTGGTAACCTACAACTGACCAGCCTGCCATCGCTGCCGCAGGGACTACAGAAGCTGT
GGGCCTATAATAATTGGCTGGCCAGCCTGCCGACGTTGCCGCCAGGACTAGGGGATCTGG
CGGTCTCTAATAACCAGCTGACCAGCCTGCCGGAGATGCCGCCAGCACTACGGGAGCTGA
GGGTCTCTGGTAACAACCTGACCAGCTGCGCGCGCTGCCGTCAGGACTACAGAAGCTGTG
GGCCTATAATAATCGGCTGACCAGCCTGCCGGAGATGTCGCCAGGACTACAGGAGCTGGA
TGTCTCTCATAACCAGCTGACCCGCCTGCCGCAAAGCCTCACGGGTCTGTCTTCAGCGGC
ACGCGTATATCTGGACGGGAATCCACTGTCTGTACGCACTCGTGACAGGCTCTGCGGACA
TCATTGGCCATTCAGGCATCAGGATACACTTCGATATGGCGGGGCCTTCCGTCCCCGGGA
AGCCCGGGCACTGCACCTGGCGGTCGCTGACTGGCTGACGTCTGCACGGGAGGGGGAAGC
GGCCCAGGCAGACAGATGGCAGGCGTTCGGACTGGAAGATAACGCCGCCGCCTTCAGCCT
GGTCCTGGACAGACTGCGTGAGACGGAAAACTTCAAAAAAGACGCGGGCTTTAAGGCACA
GATATCATCCTGGCTGACACAACTGGCTGAAGATGCTGCGCTGAGAGCAAAAACCT
TTGCCATGGCAACAGAGGCAACATCAACCTGCGAGGACCGGGTCACACATGCCCTGCACC
AGATGAATAACGTACAACTGGTACATAATGCAGAAAAAGGGGAATACGACAACAATCTCC
AGGGGCTGGTTTCCACGGGGCGTGAGATGTTCCGCCTGGCAACACTGGAACAGATTGCCC
GGGAAAAAGCCGGAACACTGGCTTTAGTCGATGACGTTGAGGTCTATCTGGCGTTCCAGA
ATAAGCTGAAGGAATCACTTGAGCTGACCAGCGTGACGTCAGAAATGCGTTTCTTTGACG
TTTCCGGCGTGACGGTTTCA
GACCTTCAGGCTGCGGACGTTCAGGTGAAAACCGCTGAAAACAGCGGGTTCAGTAAATGG
ATACTGCAGTGGGGGCCGTTACACAGCGTGCTGGAACGCAAAGTGCCGGAACGCTTTAAC
GCGCTTCGTGAAAAGCAAATATCGGATTATGAAGACACGTACCGGAAGCTGTATGACGAA
GTGCTGAAATCGTCCGGGCTGGTCGACGATACCGATGCAGAACGTACTATCGGAGTAAGT
GCGATGGATAGTGCGAAAAAAGAATTTCTGGATGGCCTGCGCGCTCTTGTGGATGAGGTG
CTGGGTAGCTATCTGACAGCCCGGTGGCGTCTTAACTGAGCACGATATTCTCCGCACCAG
GCGAATGTGGTGCGGTGAACAAAGATATTCCTTGGACAAACAACATGAGACAGCACTGAT
GATGCACAGGTGAAACAGGGGAGACTTCTTCAGTCAGGGCGTACGCAACTCAACCTTTTC
GACGATACGCGCC/
```

SEQ ID NO:16

FIG. 29

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

❏ **BLACK BORDERS**

❏ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

❏ **FADED TEXT OR DRAWING**

☑ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**

❏ **SKEWED/SLANTED IMAGES**

❏ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**

❏ **GRAY SCALE DOCUMENTS**

❏ **LINES OR MARKS ON ORIGINAL DOCUMENT**

❏ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

❏ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.